

AMSH1	THNEFTITHVIVP--KQSAGPDYCDMENVEELFNVQDQHD--LLTLGWITIPTQTAFLS
AMSH2	THNEFTITHVIVP--KQSAGPDYCDMENVEELFNVQDQHD--LLTLGWITIPTQTAFLS
AMSH	MRNEFTITHVLIP--KQSAGSDYCNTENEEELFLIQDQQG--LITLGWITIPTQTAFLS
Rpn11	TVRVIDVTFAMPQS--G/TGVSVERAVDPTFQAKMFLDMILQTRPFLMVVGWYHSHPGIGCWLS
Jabl	TMIIMDSIALFVEGTETRVNQQAAYEYMAYILENAKQVGRLENAIGNYSSPGYGCWLS
AMSH1	SVLHTHCSYQLMLPEAIAIVCSPKHKDTG----IFRITNAGMLEVSACKKGFH--PH
AMSH2	SVLHTHCSYQLMLPEAIAIVCSPKHKDTG----IFRITNAGMLEVSACKKGFH--PH
AMSH	SVLHTHCSYQMMLPEESVAIVCSPKFQETG----FFKIDOHGLEKISSCRQKGFH--PH
Rpn11	GVIINTQSFALSERAVAVVVVDPIQSVKGVVIDAFRLINANRMLVGHFRQTSNLGH
Jabl	GIVVSTQMLNQQFQEPTVAVVVDPIQSVKGVVIDAFRLINANRMLVGHFRQTSNLGH
AMSH1	TKEPRLFISICKHV--LVKDIKI-----IVLDLR-
AMSH2	TKEPRLFISIQKFLSGIISGTAL-----EMEPLKIGYGPNGFPLLGIERSSSPSEQ
AMSH	SKDPPFLCSCSHVT--VVDRAV-----TITDLR-
Rpn11	LNKPSIQALIHGLNRHYYSTITINYRKNELEQKMLLNHKKSMMEGLTLDYSEHCKHNES
Jabl	TIPLNKIEDFGVHCKQYYALEVSYFKSSLDRKLELLWNKYWNNTLSSSLITNAADYTG
AMSH1	----- L-----
AMSH2	----- VVKEMLELAKNYMKAAVEEDKMTFEQLAIKNVGKQDFKRRHLKHHVUDVILMTSNIVQCLARM
AMSH	QVEDLSEKLEQSELQLGRGSFMLG--LETHDRKSKDKLAKATRDSCKTTIEAINGLMSQV
Rpn11	----- LDTVVFK-----
Jabl	----- IKDKLFLNQINIS

FIGURE 1

AMSH1	-----MPDHDVSLSPEERVRALSKLGCNITISEDITPRR	35
AMSH2	MDQPTTVNSLKKLAAMPDHTDVSLSPEERVRALSKLGCNITISEDITPRR	50
AMSH	-----MSDRGDSLPPEDRVRALSQLGSAVEVNEDIPPRR	35
	*****	*****
AMSH1	YFRSGVEMERMASVYLEEGNLENAFVLYNKFITLVEVKLPNHRDYQQCAV	85
AMSH2	YFRSGVEMERMASVYLEEGNLENAFVLYNKFITLVEVKLENHRDYQQCAV	100
AMSH	YFRSGVIIIRMASIYSEEGNIEHAJFLYNEYITLFLKLLPKHRDYKSAVI	85
	*****	*****
AMSH1	PEKQDIMKKLKEIAFPRTDELKNDLKKYKNEYQEYLQSKNKKAEILKK	135
AMSH2	PEKQDIMKKLKEIAFPRTDELKNDLKKYKNEYQEYLQSKNKKAEILKK	150
AMSH	PEKQDITVKKLKEIAFPKAKEIKAAELLERYTKEYTEYNEEKKKEAELARN	135
	*****	*****
AMSH1	LEHQRLLIEAERKRIAQMRCQQQLSEQFLFFEDQLKKQE LARGQ MRSQQTS	185
AMSH2	LEHQRLLIEAERKRIAQMRCQQQLSEQFLFFEDQLKKQE LARGQ MRSQQTS	200
AMSH	MAIQQELEKEKQRAQQKQQQLQEQLQHAEEMIRNQE LERERLKIVQEF	185
	*****	*****
AMSH1	G-LSEQIDGSALS CFS--THQNNSLNVFADQPNKSDATNYASHSPPVNR	232
AMSH2	G-LSEQIDGSALS CFS--THQNNSLNVFADQPNKSDATNYASHSPPVNR	247
AMSH	GKVDDEGLGGPLVPDFLEKPSLDVFPTLT VSSIQPSDCHTTVRPAKPPVDR	235
	*****	*****
AMSH1	ALTPAATLSAVQN LVVEGLRCVV LPEDLCHKF LQLAESNTVRGIETCGIL	262
AMSH2	ALTPAATLSAVQN LVVEGLRCVV LPEDLCHKF LQLAESNTVRGIETCGIL	297
AMSH	SLKPGALSNSESIPTIDGLRHVVVVGRLCPQFLQLASANTARGVETCGIL	285
	*****	*****
AMSH1	CGKLITHNEFTIITHVIVPKQSAGPDYCDMENVEELFNVQDQHDLLTLGWII	332
AMSH2	CGKLITHNEFTIITHVIVPKQSAGPDYCDMENVEELFNVQDQHDLLTLGWII	347
AMSH	CGKLMRNEFTIITHVLIPKQSAGSDYCMTENEELFLIQDQQGLLTLGWI	335
	*****	*****
AMSH1	TPTQTAFLSSVILHITHCSYQIMLPEAI AIVCSPKHKDTGIFRLINAGML	382
AMSH2	TPTQTAFLSSVILHITHCSYQIMLPEAI AIVCSPKHKDTGIFRLINAGML	397
AMSH	TPTQTAFLSSVILHITHCSYQIMLPESVAVIIVCSPKFQETGFIFKLTDBGLE	385
	*****	*****
AMSH1	EVSACKKKGIFHPTKIPRLFSICKHV--LVKDIKIIVLDLR-----	421
AMSH2	EVSACKKKGIFHPTKIPRLFSIQKFLSGIISGTALEMPLXIGYGPNGFP	447
AMSH	EISSCRQKGIFHPSKDPPFLCSCSHVT--VVDRAVITDLR-----	424
	*****	*****
AMSH1	-----	
AMSH2	LLGIISRSSSPSEQL	461
AMSH	-----	

FIGURE 2

COP9_su5_Hs
COP9_su5_Dm
COP9_su5_At
COP9_su5_Ce
AF2198_Arcfu
PH0451_Pyrho
TVN1035_Thevo
MTH971_Meth
aq_1691_Aquae
RV1334_Myctu
RadC_Ecoli

VGRLENAIGWYHSHPGYGCWLSGIDVSTQMLNQQFQEPFVA--VVIDPTRTI SAGKVNLG
VGRMEHAVGWHYHSHPGYGCWLSGINVSTQMLNQTYQEPFVA--IVVDPVRTVSAGKVCLG
AGRLENVGWYHSHPGYGCWLSGIDVSTQRLNQQHQEPFLA--VVIDPTRTVSAGKVEIG
EGRKEKVVGVWYHSHPGYGCWLSGIDVSTQTLNQKFQEPWVA--IVIDPLRTMSAGKVDIG
LPIGMKVFGTVHSHPSPSCRPEEDLSLFTRFGKYHIIVCY--PYDENSWKCYNRKGEEV
MPHDESIKGTFHSHPSPPYPSEGDLMFFSKFGGIHIIIAAF--PYDEDSVKAFDSEGREV
KPIDFSLVGSVHSHPSGITKPSDEDLRMFSLTGKIHIIVGY--PYNLKDYSAYDRSGNKV
LPPFTGAVGSVHSHPGPVNLPSSAADLHFFSKNGLFHLLIAH--PYTMETVAAYTRNGDPV
ISKGMEIVGVYHSHPDHPDRPSQFDLQRRAFPDLSYIIFSVQ--KGKVASYRSWELKGDKF
EDADEVPVVIYHSHTATEAYPSRTDVKLATEPDHYVLVSTRDPRHELRSYRIVDGAVT
IKINASALILAHNHPSGCAEPSKADKLITERIIKSCQFMDL--RVLDHIVIGRGEYVSFA
.....HSHP'....S'D

FIGURE 3

COP9_sus5_Hs VGRLENAIGWYHSHPGYGCWLSGIDVSTQMLNQQFQEPFVA--VVVIDPTRTI SAGKVNLG
COP9_sus5_Dm VGRMEHAVGWYHSHPGYGCWLSGINVSTQMLNOTYQEPFVA--IVVDPVRTVSAGKVCLG
COP9_sus5_At AGRLENVVGWYHSHPGYGCWLSGIDVSTQRLNQQHQEPFLA--VVVIDPTRTVSAGKVBIG
COP9_sus5_Ce EGRKEKVVGVWYHSHPGYGCWLSGIDVSTQTLNQKFQEPWVA--IVIDPLRTMSAGKVDIG
Pad1_Dm TGRPEMVGWYHSHPGFGCWLSGVDINTQQSFEALSERAVA--VVVDPIQSVKG-KVVID
Pad1_Hs TGRPEMVGWYHSHPGFGCWLSGVDINTQQSFEALSERAVA--VVVDPIQSVKG-KVVID
Sks1_Dd TGRDEIVIGWYHSHPGFGCWLSGVDNTQQSFEQLQSRAVA--VVVDPLQSVRG-KVVID
Pad1_Sc TGRDQMVGWYHSHPGFGCWLSGVDNTQKSFEQLNSRAVA--VVVDPIQSVKG-KVVID
..... HSHP.....'S 'D

FIGURE 4